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PCT10

RAW SEQUENCE LISTING   DATE: 08/05/2002
PATENT APPLICATION: US/10/049,822   TIME: 11:34:53

Input Set : **A:\OHTA SEQUENCE LISTING (Final Copy).txt**
Output Set: **N:\CRF3\08052002\J049822.raw**

Does Not Comply
Corrected Diskette Needed

```
 3  <110> APPLICANT: OHTA, Shigeo
 4          ASOH, Sadamitsu
 6  <120> TITLE OF INVENTION: A GENETICALLY ENGINEERED cDNA OF RAT bcl-x GENE AND AN
IMPROVED
 7          PROTEIN
 9  <130> FILE REFERENCE: 2002-0256A/LC/00653
11  <140> CURRENT APPLICATION NUMBER: 10/049,822
12  <141> CURRENT FILING DATE: 2002-04-01
14  <150> PRIOR APPLICATION NUMBER: PCT/JP00/05502
15  <151> PRIOR FILING DATE: 2000-08-17
17  <150> PRIOR APPLICATION NUMBER: JP11-230642
18  <151> PRIOR FILING DATE: 1999-08-17
20  <160> NUMBER OF SEQ ID NOS: 17
22  <170> SOFTWARE: PatentIn Ver. 2.1
24  <210> SEQ ID NO: 1
25  <211> LENGTH: 1742
26  <212> TYPE: DNA
27  <213> ORGANISM: Rattus norvegicus
29  <220> FEATURE:
30  <221> NAME/KEY: CDS
31  <222> LOCATION: (72)..(773)
33  <300> PUBLICATION INFORMATION:
34  <302> TITLE: An additional form of rat Bcl-x, Bcl-xbeta, generated
35          by an unspliced RNA, promotes apoptosis in promyeloid
36          cells.
37  <303> JOURNAL: J. Biol. Chem.
38  <304> VOLUME: 271
39  <305> ISSUE: 22
40  <306> PAGES: 13258-13265
41  <307> DATE: 1996-05-31
43  <400> SEQUENCE: 1
44  cacagagcag acccagtgag tgagcaggtg ttttggacaa tggactgttt gagcccatct  60
45  ctattataaa a atg tct cag agc aac cgg gag ctg gtg gtt gac ttt ctc  110
46               Met Ser Gln Ser Asn Arg Glu Leu Val Val Asp Phe Leu
47                 1               5                   10
48  tcc tac aag ctc tcc cag aaa gga tac agc tgg agt cag ttt agc gat  158
                   Ser Tyr Lys Leu Ser Gln Lys Gly Tyr Ser Trp Ser Gln Phe Ser Asp
```

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: _/5/549,?cc_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ___ Wrapped Nucleics
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 ___ Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ___ Misaligned Amino
Numbering

The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use **space characters**, instead.

4 ___ Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**

5 ___ Variable Length

Sequence(s)___contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ___ PatentIn 2.0
"bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7 ___ Skipped Sequences
(OLD RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 ___ Skipped Sequences
(NEW RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 ___ Use of n's or Xaa's
(NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 ___ Invalid <213>
Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 ___ Use of <220>

Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12 ___ PatentIn 2.0
"bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ___ Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

(handwritten: (11./21./)

(handwritten top right: IN 50(C)

(handwritten: 50CO)

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: *10/049,822*
Source: *PCT/10*
Date Processed by STIC: *8/5/2002*

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
   http://www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
   U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
          Or

Federal Express, United Parcel Service, or other courier service
Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

RAW SEQUENCE LISTING   DATE: 08/05/2002
PATENT APPLICATION: US/10/049,822   TIME: 11:34:53

Input Set : A:\OHTA SEQUENCE LISTING (Final Copy).txt
Output Set : N:\CRF3\08052002\J049822.raw

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57 agc ccc gcg gtg aat gga gcc act ggc cac agc agc agt ttg gat gcg   302
58 Ser Pro Ala Val Asn Gly Ala Thr Gly His Ser Ser Ser Leu Asp Ala
59          65                  70                  75
60 cgg gag gta atc ccc atg gca gca gtg aag caa gcg ctg aga gag gct   350
61 Arg Glu Val Ile Pro Met Ala Ala Val Lys Gln Ala Leu Arg Glu Ala
62          80                  85                  90
63 ggc gat gag ttt gaa ctg cgg tac cgg aga gca ttc agt gat cta aca   398
64 Gly Asp Glu Phe Glu Leu Arg Tyr Arg Arg Ala Phe Ser Asp Leu Thr
65       95                  100                 105
66 tcc cag ctt cat ata acc cca ggg aca gca tat cag agc ttt gaa cag   446
67 Ser Gln Leu His Ile Thr Pro Gly Thr Ala Tyr Gln Ser Phe Glu Gln
68 110             115                 120                 125
69 gta gtg aat gaa ctc ttt cgg gat ggg gta aac tgg ggt cgc att gtg   494
70 Val Val Asn Glu Leu Phe Arg Asp Gly Val Asn Trp Gly Arg Ile Val
71              130                 135                 140
72 gcc ttc ttc tcc ttt ggc ggg gca ctg tgc gtg gaa agc gta gac aag   542
73 Ala Phe Phe Ser Phe Gly Gly Ala Leu Cys Val Glu Ser Val Asp Lys
74              145                 150                 155
75 gag atg cag gta ttg gtg agt cgg att gca agt tgg atg gcc acc tac   590
76 Glu Met Gln Val Leu Val Ser Arg Ile Ala Ser Trp Met Ala Thr Tyr
77          160                 165                 170
78 ctg aat gac cac cta gag cct tgg atc cag gag aac ggc ggc tgg gac   638
79 Leu Asn Asp His Leu Glu Pro Trp Ile Gln Glu Asn Gly Gly Trp Asp
80       175                 180                 185
81 act ttt gtg gat ctc tac ggg aac aat gca gca gcc gag agc cgg aaa   686
82 Thr Phe Val Asp Leu Tyr Gly Asn Asn Ala Ala Ala Glu Ser Arg Lys
83 190             195                 200                 205
84 ggc cag gag cgt ttc aac cgc tgg ttc ctg acg ggc atg act gtg gct   734
85 Gly Gln Glu Arg Phe Asn Arg Trp Phe Leu Thr Gly Met Thr Val Ala
86              210                 215                 220
87 ggt gta gtt ctg ctg ggc tca ctc ttc agt cgg aag tga ccagacactg   783
88 Gly Val Val Leu Leu Gly Ser Leu Phe Ser Arg Lys
89              225                 230
90 accgtccact cacctctcac ctcccacctt gccccacca caactctctc ttcagccacc 843
91 attgctacaa gggagaaccac tacatgcaac tcaagccct tcccctatta tagggttggg 903
92 cctagacgga gtccctgca gttagcttto tagaatctac cacgcttctg tgaaagccac 963
93 cttcccccca catctcagtt tccttggcct caaatctcac aaggttttc ctcagatcag 1023
94 ctccttggag gctggcagga ttattaaggg gtgt ctaga ggggagaagag cctgccttgt 1083
95 tggtgggagc ctgattaccc ctgaggctct cgggaatgct tttctggcag gggagctggag 1143
96 agctctctaa acctcttccc ccagagacta gattgccttg gtttttgatgt gtgtggcctc 1203
97 agaattgatc catttccat tctgctgtgt ccctggggcg gctcctcctt cccatctcca 1263
98 ccccccccc cccagagcca ttgagtgagg tgcttttagc ccttttgact aactaaaaat 1323
99 gcaggctgct tgggataacg aggcaaggac ctcctcccca cctgtggcct ggccaagccc 1383
100 ccactcctgg tctgaatgtt ctcctgaggc ctctggctag agtccagccc cacccagcag 1443
101 gaggggacgga gctgcggaaa gtccacccta cgagagcctg agcggctctt gcgggcttagc 1503
102 ............. .......... ........... tggctccatg gtgaccatga ctgagggacc 1563
```

```
108 <210> SEQ ID NO: 2
109 <211> LENGTH: 233
110 <212> TYPE: PRT
111 <213> ORGANISM  Rattus norvegicus
113 <400> SEQUENCE: 2
114 Met Ser Gln Ser Asn Arg Glu Leu Val Val Asp Phe Leu Ser Tyr Lys
115   1               5               10              15
116 Leu Ser Gln Lys Gly Tyr Ser Trp Ser Gln Phe Ser Asp Val Glu Glu
117             20              25              30
118 Asn Arg Thr Glu Ala Pro Glu Glu Thr Glu Pro Glu Arg Glu Thr Pro
119         35              40              45
120 Ser Ala Ile Asn Gly Asn Pro Ser Trp His Leu Ala Asp Ser Pro Ala
121     50              55              60
122 Val Asn Gly Ala Thr Gly His Ser Ser Ser Leu Asp Ala Arg Glu Val
123 65              70              75              80
124 Ile Pro Met Ala Ala Val Lys Gln Ala Leu Arg Glu Ala Gly Asp Glu
125             85              90              95
126 Phe Glu Leu Arg Tyr Arg Arg Ala Phe Ser Asp Leu Thr Ser Gln Leu
127             100             105             110
128 His Ile Thr Pro Gly Thr Ala Tyr Gln Ser Phe Glu Gln Val Val Asn
129         115             120             125
130 Glu Leu Phe Arg Asp Gly Val Asn Trp Gly Arg Ile Val Ala Phe Phe
131     130             135             140
132 Ser Phe Gly Gly Ala Leu Cys Val Glu Ser Val Asp Lys Glu Met Gln
133 145             150             155             160
134 Val Leu Val Ser Arg Ile Ala Ser Trp Met Ala Thr Tyr Leu Asn Asp
135             165             170             175
136 His Leu Glu Pro Trp Ile Gln Glu Asn Gly Gly Trp Asp Thr Phe Val
137         180             185             190
138 Asp Leu Tyr Gly Asn Asn Ala Ala Ala Glu Ser Arg Lys Gly Gln Glu
139         195             200             205
140 Arg Phe Asn Arg Trp Phe Leu Thr Gly Met Thr Val Ala Gly Val Val
141     210             215             220
142 Leu Leu Gly Ser Leu Phe Ser Arg Lys
143 225                 230

145 <210> SEQ ID NO: 3
146 <211> LENGTH: 233
147 <212> TYPE: PRT
148 <213> ORGANISM: (Modified protein
150 <400> SEQUENCE: 3
151 Met Ser Gln Ser Asn Arg Glu Leu Val Val Asp Phe Leu Ser Tyr Lys
152   1               5               10              15
153 Leu Ser Gln Lys Gly Phe Ser Trp Ser Asn Phe Ser Asp Val Glu Glu
154             20              25              30
155 Asn Arg Thr Gln Ala Pro Glu Glu Thr Glu Pro Glu Arg Glu Thr Pro
                        40              45
```

RAW SEQUENCE LISTING   DATE: 08/05/2002
PATENT APPLICATION: US/10/049,822 TIME: 11:34:53

Input Set A:\OHTA SEQUENCE LISTING (Final Copy).txt
Output Set N:\CRF3\08052002\J049822.raw

```
160  65                    70                  75                    80
161 Ile Pro Met Ala Ala Val Lys Gln Ala Leu Arg Glu Ala Gly Asp Glu
162             85                  90                  95
163 Phe Glu Leu Arg Tyr Arg Arg Ala Phe Ser Asp Leu Thr Ser Gln Leu
164             100                 105                 110
165 His Ile Thr Pro Gly Thr Ala Tyr Gln Ser Phe Glu Gln Val Val Asn
166             115                 120                 125
167 Glu Leu Phe Arg Asp Gly Val Asn Trp Gly Arg Ile Val Ala Phe Phe
168         130                 135                 140
169 Ser Phe Gly Gly Ala Leu Cys Val Glu Ser Val Asp Lys Glu Met Gln
170 145                 150                 155                 160
171 Val Leu Val Ser Lys Ile Ala Ser Trp Met Ala Thr Tyr Leu Asn Asp
172                 165                 170                 175
173 His Leu Glu Pro Trp Ile Gln Glu Asn Gly Gly Trp Asp Thr Phe Val
174         180                 185                 190
175 Asp Leu Tyr Gly Asn Asn Ala Ala Ala Glu Ser Arg Lys Gly Gln Glu
176         195                 200                 205
177 Arg Phe Asn Arg Trp Phe Leu Thr Gly Met Thr Val Ala Gly Val Val
178     210                 215                 220
179 Leu Leu Gly Ser Leu Phe Ser Arg Lys
180 225                 230
183 <210> SEQ ID NO: 4
184 <211> LENGTH: 26
185 <212> TYPE: DNA
186 <213> ORGANISM: Artificial sequence
188 <220> FEATURE:
189 <223> OTHER INFORMATION: Artificial sequence: Synthesized oligonucleotide
191 <220> FEATURE:
```

W--> 192 <221> NAME/KEY: base
```
193 <222> LOCATION: (1)
194 <222> LOCATION: n = a, c, t or g
196 <220> FEATURE:
```
W--> 197 <221> NAME/KEY: base
```
198 <222> LOCATION: (2)
```
W--> 199 <222> n = a, c, t or g
W--> 201 <220> FEATURE:
W--> 202 <221> NAME/KEY: base
```
203 <222> LOCATION: (3)
```
W--> 204 <222> n = a, c, t or g
W--> 206 <220> FEATURE:
W--> 207 <221> NAME/KEY: base
```
208 <222> LOCATION: (4)
```
W--> 209 <222> n = a, c, t or g
W--> 211 <220> FEATURE:
W--> 212 <221> NAME/KEY: base
```
                     LOCATION: (5)
```

RAW SEQUENCE LISTING   DATE: 08/05/2002
PATENT APPLICATION   US/10/049,822   TIME: 11:34:53

Input Set : A:\OHTA SEQUENCE LISTING (Final Copy).txt
Output Set: N:\CRF3\08052002\J049822.raw

```
       218 <222> LOCATION: (6)
W--> 219 <222> n = a, c, t or g
W--> 221 <400> 4
W--> 222 nnnnnnacta gtggatcctg gaagag                    26
       225 <210> SEQ ID NO: 5
       226 <211> LENGTH: 28
       227 <212> TYPE: DNA
       228 <213> ORGANISM: Artificial sequence
       230 <220> FEATURE:
       231 <223> OTHER INFORMATION: Artificial sequence: Synthesized oligonucleotide
       233 <400> SEQUENCE: 5
       234 gcaatcttac tcaccaatac ctgcatct                 28
       237 <210> SEQ ID NO: 6
       238 <211> LENGTH: 27
       239 <212> TYPE: DNA
       240 <213> ORGANISM: Artificial sequence
       242 <220> FEATURE:
       243 <223> OTHER INFORMATION: Artificial sequence: Synthesized oligonucleotide
       245 <400> SEQUENCE: 6
       246 ggtgagtaag attgcaagtt ggatggc                  27
       249 <210> SEQ ID NO: 7
       250 <211> LENGTH: 19
       251 <212> TYPE: DNA
       252 <213> ORGANISM: Artificial sequence
       254 <220> FEATURE:
       255 <223> OTHER INFORMATION: Artificial sequence: Synthesized oligonucleotide
       257 <400> SEQUENCE: 7
       258 tcctggatcc aaggctcta                           19
       261 <210> SEQ ID NO: 8
       262 <211> LENGTH: 28
       263 <212> TYPE: DNA
       264 <213> ORGANISM: Artificial sequence
       266 <220> FEATURE:
       267 <223> OTHER INFORMATION: Artificial sequence: Synthesized oligonucleotide
       269 <400> SEQUENCE: 8
       270 actaaagtta ctccagctgt atcctttc                 28
       272 <210> SEQ ID NO: 9
       273 <211> LENGTH: 31
       275 <212> TYPE: DNA
       276 <213> ORGANISM: Artificial sequence
       278 <220> FEATURE:
       279 <223> OTHER INFORMATION: Artificial sequence: Synthesized oligonucleotide
       281 <400> SEQUENCE: 9
       282 ctggagtaac tttagccatg tccaagacaa c             31
       284 <210> SEQ ID NO: 10
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 08/05/2002
PATENT APPLICATION: US/10/049,822   TIME: 11:34:54

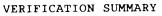Input Set : A:\OHTA SEQUENCE LISTING (Final Copy).txt
Output Set: N:\CRF3\08052002\J049822.raw

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:4; N Pos. 1,2,3,4,5,6
Seq#:15; N Pos. 1,2,3,4
Seq#:17; N Pos. 1,2,3,4,5,6,7,8

VERIFICATION SUMMARY   DATE: 08/05/2002
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Input Set : A:\OHTA SEQUENCE LISTING (Final Copy).txt
Output Set: N:\CRF3\08052002\J049822.raw

```
L:192 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:197 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:199 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:4
L:202 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:204 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:4
L:207 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:209 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:4
L:212 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:214 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:4
L:217 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:219 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:4
L:221 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:4
L:222 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0
L:349 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:15
L:354 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:15
L:356 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:15
L:359 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:15
L:361 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:15
L:364 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:15
L:366 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:15
L:369 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:15
L:370 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:0
L:392 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:17
L:397 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:17
L:399 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:17
L:402 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:17
L:404 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:17
L:407 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:17
L:409 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:17
L:412 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:17
L:414 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:17
L:417 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:17
L:419 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:17
L:422 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:17
L:424 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:17
L:427 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:17
L:429 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:17
L:431 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:17
L:432 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:0
```